

(1) GENERAL INFORMATION:

(ii) TITLE OF INVENTION: Inward Rectifier, G-Protein Activated, Mammalian, Potassium Channels and Uses Thereof

(iv) CORRESPONDENCE ADDRESS:

(v) COMPUTER READABLE FORM:

(vi) CURRENT APPLICATION DATA:

(viii) ATTORNEY/AGENT INFORMATION:

(ix) TELECOMMUNICATION INFORMATION:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA 52  
Met Ser Ala Leu Arg Arg Lys  
1 5

TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC 100  
Phe Gly Asp Tyr Gln Val Thr Thr Ser Ser Ser Gly Ser Gly  
10 15 20

TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC 148  
Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro  
25 30 35

AAG Lys 40	AAG Lys	AAA Lys	CGG Arg	CGG Gln	CGG Arg 45	TTC Phe	GTG Val	GAC Asp	AAG Lys	AAC Asn 50	GGT Gly	CGG Arg	TGC Cys	AAT Asn	GTG Val 55	196
CAG Gln	CAC His	GGC Gly	AAC Asn	CTG Leu 60	GGC Gly	AGC Ser	GAG Glu	ACC Thr	AGT Ser 65	CGC Arg	TAC Tyr	CTT Leu	TCC Ser	GAC Asp 70	CTC Leu	244
TTC Phe	ACT Thr	ACC Thr	CTG Leu 75	GTG Val	GAT Asp	CTC Leu	AAG Lys	TGG Trp 80	CGT Arg	TGG Trp	AAC Asn	CTC Leu	TTT Phe 85	ATC Ile	TTC Phe	292
ATC Ile	CTC Leu	ACC Thr 90	TAC Tyr	ACC Thr	GTG Val	GCC Ala	TGG Trp 95	CTC Leu	TTC Phe	ATG Met	GCG Ala	TCC Ser 100	ATG Met	TGG Trp	TGG Trp	340
GTG Val 105	ATC Ile	GCT Ala	TAT Tyr	ACC Thr	CGG Arg	GGC Gly 110	GAC Asp	CTG Leu	AAC Asn	AAA Lys	GCC Ala 115	CAT His	GTC Val	GGC Gly	AAC Asn	388
TAC Tyr 120	ACT Thr	CCC Pro	TGT Cys	GTG Val	GCC Ala 125	AAT Asn	GTC Val	TAT Tyr	AAC Asn	TTC Phe 130	CCC Pro	TCT Ser	GCC Ala	TTC Phe	CTT Leu 135	436
TTC Phe	TTC Phe	ATC Ile	GAG Glu	ACC Thr 140	GAG Glu	GCC Ala	ACC Thr	ATC Ile	GGC Gly 145	TAT Tyr	GGC Gly	TAC Tyr	CGC Arg	TAC Tyr 150	ATC Ile	484
ACC Thr	GAC Asp	AAG Lys	TGC Cys 155	CCC Pro	GAG Glu	GGC Gly	ATC Ile	ATC Ile 160	CTT Leu	TTC Phe	CTT Leu	TTC Phe	CAG Gln 165	TCC Ser	ATC Ile	532
CTT Leu	GGC Gly	TCC Ser 170	ATC Ile	GTG Val	GAC Asp	GCT Ala	TTC Phe 175	CTC Leu	ATC Ile	GGC Gly	TGC Cys	ATG Met 180	TTC Phe	ATC Ile	AAG Lys	580
ATG Met 185	TCC Ser	CAG Gln	CCC Pro	AAA Lys	AAG Lys	CGC Arg 190	GCC Ala	GAG Glu	ACC Thr	CTC Leu	ATG Met 195	TTT Phe	AGC Ser	GAG Glu	CAT His	628
GCG Ala 200	GTT Val	ATT Ile	TCC Ser	ATG Met	AGG Arg 205	GAC Asp	GGA Gly	AAA Lys	CTC Leu	ACT Thr 210	CTC Leu	ATG Met	TTC Phe	CGG Arg	GTG Val 215	676
GGC Gly	AAC Asn	CTG Leu	CGC Arg	AAC Asn 220	AGC Ser	CAC His	ATG Met	GTC Val	TCC Ser 225	GCG Ala	CAG Gln	ATC Ile	CGC Arg	TGC Cys 230	AAG Lys	724
CTG Leu	CTC Leu	AAA Lys	TCT Ser 235	CGG Arg	CAG Gln	ACA Thr	CCT Pro	GAG Glu 240	GGT Gly	GAG Glu	TTT Phe	CTA Leu	CCC Pro 245	CTT Leu	GAC Asp	772
CAA Gln	CTT Leu	GAA Glu 250	CTG Leu	GAT Asp	GTA Val	GGT Gly	TTT Phe 255	AGT Ser	ACA Thr	GGG Gly	GCA Ala 260	GAT Asp 260	CAA Gln	CTT Leu	TTT Phe	820
CTT Leu	GTG Val 265	TCC Ser	CCT Pro	CTC Leu	ACC Thr	ATT Ile 270	TGC Cys	CAC His	GTG Val	ATC Ile	GAT Asp 275	GCC Ala	AAA Lys	AGC Ser	CCC Pro	868
TTT Phe 280	TAT Tyr	GAC Asp	CTA Leu	TCC Ser	CAG Gln 285	CGA Arg	AGC Ser	ATG Met	CAA Gln	ACT Thr 290	GAA Glu	CAG Gln	TTC Phe	GAG Glu	GTG Val 295	916
GTC Val	GTC Val	ATC Ile	CTG Leu	GAA Glu 300	GGC Gly	ATC Ile	GTG Val	GAA Glu 305	ACC Thr	ACA Thr	GGG Gly	ATG Met	ACT Thr 310	TGT Cys	CAA Gln	964



(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr  
1 5 10 15  
Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly  
20 25 30  
Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp  
35 40 45  
Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr  
50 55 60  
Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp  
65 70 75 80  
Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu  
85 90 95  
Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu  
100 105 110  
Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr  
115 120 125  
Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile  
130 135 140  
Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile  
145 150 155 160  
Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu  
165 170 175  
Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu  
180 185 190  
Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys  
195 200 205  
Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val  
210 215 220  
Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu  
225 230 235 240  
Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser  
245 250 255  
Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His  
260 265 270  
Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met  
275 280 285  
Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu  
290 295 300  
Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu  
305 310 315 320

09039927 034699

[illegible]